

SEQUENCE LISTING



<110> SAITOH, Shuji  
TSUZAKI, Yoshinari  
YANAGIDA, Noboru

<120> NOVEL FUSED PROTEIN, GENE THEREFOR, RECOMBINANT VECTOR,  
RECOMBINANT VIRUS, AND ITS USE

<130> 981167

<140> 09/147,052

<141> 1999-04-05

<150> JP 08-103548

<151> 1996-03-29

<150> PCT/JP97/01084

<151> 1997-03-28

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 1371

<212> DNA

<213> hybrid

<400> 1

```

atgcactatt ttaggcggaa ttgcatatTT ttccttatag ttattctata tggtagaac 60
tcatctccga gtacccaaaa tgtgacatca agagaagttg ttctgagcgt ccagttgtct 120
gaggaagagt ctacgtttta tctttgtccc ccaccagtgg gttcaaccgt gatccgtcta 180
gaattcgggt gtatgtctat tactaaaaaa gatgcaaacc caaataatgg ccaaacccaa 240
ttagaagcag cgcgaaatga gttaacagat ctaatcaatg ctaaagcgat gacattagct 300
tactacaag actatgccaa gattgaagct agtttatcat ctgcttatag tgaagctgaa 360
acagttaaca ataaccttaa tgcaacatta gaacaactaa aaatggctaa aactaattta 420
gaatcagcca tcaaccaagc taatacggat aaaacgactt ttgataatga acacccaaat 480
ttagttgaag catacaaagc actaaaaacc actttagaac aacgtgctac taaccttgaa 540
ggtttgtcat caactgctta taatcaaatt cgcaataatt tagtgatct atacaataaa 600
gctagtagtt taataactaa aacactagat ccactaaatg ggggaacgct ttagattct 660
aatgagatta ctacagctaa taagaatatt aataatacgt tatcaactat taatgaacaa 720
aagactaatg ctgatgcatt atctaatagt tttattaaaa aagtgattca aaataatgaa 780
caaagttttg tagggacttt tacaaacgct aatgttcaac cttcaaacta cagttttgtt 840
gcttttagtg ctgatgtaac acccgtcaat tataaatatg caagaaggac cgtttggaat 900
ggtgatgaac cttcaagtag aattcttgca aacacgaata gtatcacaga tgtttcttgg 960
atttatagtt tagctggaac aaacacgaag taccaattta gttttagcaa ctatggtcca 1020
tcaactgggtt atttatatTT cccttataag ttggttaaag cagctgatgc taataacggt 1080

```

ggattacaat acaaattaaa taatggaaat gttcaacaag ttgagtttgc cacttcaact 1140  
 agtgcaaata atactacagc taatccaact ccagcagttg atgagattaa agttgctaaa 1200  
 atcgttttat caggtttaag atttggccaa aacacaatcg aattaagtgt tccaacgggt 1260  
 gaaggaaata tgaataaagt tgcgccaatg attggcaaca tttatcttag ctcaaataa 1320  
 aataatgctg ataagatccc cgggtaccgt cgaccggta cattttata a 1371

<210> 2

<211> 456

<212> PRT

<213> hybrid

<400> 2

Met His Tyr Phe Arg Arg Asn Cys Ile Phe Phe Leu Ile Val Ile Leu  
 1 5 10 15

Tyr Gly Thr Asn Ser Ser Pro Ser Thr Gln Asn Val Thr Ser Arg Glu  
 20 25 30

Val Val Ser Ser Val Gln Leu Ser Glu Glu Glu Ser Thr Phe Tyr Leu  
 35 40 45

Cys Pro Pro Pro Val Gly Ser Thr Val Ile Arg Leu Glu Phe Gly Cys  
 50 55 60

Met Ser Ile Thr Lys Lys Asp Ala Asn Pro Asn Asn Gly Gln Thr Gln  
 65 70 75 80

Leu Glu Ala Ala Arg Met Glu Leu Thr Asp Leu Ile Asn Ala Lys Ala  
 85 90 95

Met Thr Leu Ala Ser Leu Gln Asp Tyr Ala Lys Ile Glu Ala Ser Leu  
 100 105 110

Ser Ser Ala Tyr Ser Glu Ala Glu Thr Val Asn Asn Asn Leu Asn Ala  
 115 120 125

Thr Leu Glu Gln Leu Lys Met Ala Lys Thr Asn Leu Glu Ser Ala Ile  
 130 135 140

Asn Gln Ala Asn Thr Asp Lys Thr Thr Phe Asp Asn Glu His Pro Asn  
 145 150 155 160

Leu Val Glu Ala Tyr Lys Ala Leu Lys Thr Thr Leu Glu Gln Arg Ala  
 165 170 175

Thr Asn Leu Glu Gly Leu Ser Ser Thr Ala Tyr Asn Gln Ile Arg Asn  
 180 185 190

Asn	Leu	Val	Asp	Leu	Tyr	Asn	Lys	Ala	Ser	Ser	Leu	Ile	Thr	Lys	Thr	195	200	205	
Leu	Asp	Pro	Leu	Asn	Gly	Gly	Thr	Leu	Leu	Asp	Ser	Asn	Glu	Ile	Thr	210	215	220	
Thr	Ala	Asn	Lys	Asn	Ile	Asn	Asn	Thr	Leu	Ser	Thr	Ile	Asn	Glu	Gln	225	230	235	240
Lys	Thr	Asn	Ala	Asp	Ala	Leu	Ser	Asn	Ser	Phe	Ile	Lys	Lys	Val	Ile	245	250	255	
Gln	Asn	Asn	Glu	Gln	Ser	Phe	Val	Gly	Thr	Phe	Thr	Asn	Ala	Asn	Val	260	265	270	
Gln	Pro	Ser	Asn	Tyr	Ser	Phe	Val	Ala	Phe	Ser	Ala	Asp	Val	Thr	Pro	275	280	285	
Val	Asn	Tyr	Lys	Tyr	Ala	Arg	Arg	Thr	Val	Trp	Asn	Gly	Asp	Glu	Pro	290	295	300	
Ser	Ser	Arg	Ile	Leu	Ala	Asn	Thr	Asn	Ser	Ile	Thr	Asp	Val	Ser	Trp	305	310	315	320
Ile	Tyr	Ser	Leu	Ala	Gly	Thr	Asn	Thr	Lys	Tyr	Gln	Phe	Ser	Phe	Ser	325	330	335	
Asn	Tyr	Gly	Pro	Ser	Thr	Gly	Tyr	Leu	Tyr	Phe	Pro	Tyr	Lys	Leu	Val	340	345	350	
Lys	Ala	Ala	Asp	Ala	Asn	Asn	Val	Gly	Leu	Gln	Tyr	Lys	Leu	Asn	Asn	355	360	365	
Gly	Asn	Val	Gln	Gln	Val	Glu	Phe	Ala	Thr	Ser	Thr	Ser	Ala	Asn	Asn	370	375	380	
Thr	Thr	Ala	Asn	Pro	Thr	Pro	Ala	Val	Asp	Glu	Ile	Lys	Val	Ala	Lys	385	390	395	400
Ile	Val	Leu	Ser	Gly	Leu	Arg	Phe	Gly	Gln	Asn	Thr	Ile	Glu	Leu	Ser	405	410	415	
Val	Pro	Thr	Gly	Glu	Gly	Asn	Met	Asn	Lys	Val	Ala	Pro	Met	Ile	Gly	420	425	430	
Asn	Ile	Tyr	Leu	Ser	Ser	Asn	Glu	Asn	Asn	Ala	Asp	Lys	Ile	Pro	Gly	435	440	445	

Tyr Arg Arg Pro Gly Thr Phe Leu  
 450 455

<210> 3  
 <211> 3261  
 <212> DNA  
 <213> hybrid

<400> 3  
 atgcactatt ttaggcggaa ttgcatat ttccttatag ttattctata tggtagaac 60  
 tcatctccga gtacccaaaa tgtgacatca agagaagttg tttcgagcgt ccagttgtct 120  
 gaggaagagt ctacgtttta tctttgtccc ccaccagtgg gttcaaccgt gatccgtcta 180  
 gaaccgccgc gaaaatgtcc cgaacctaga aaagccaccg agtggggtga aggaatcgcg 240  
 atattattta aagagaatat cagtccatat aaattttaaag tgacgcttta ttataaaaat 300  
 atcattcaga cgacgacatg gacggggacg acatatagac agatcactaa tcgatataca 360  
 gataggacgc ccgtttccat tgaagagatc acggatctaa tcgacggcaa aggaagatgc 420  
 tcatctaaag caagatacct tagaaacaat gtatatgttg aagcgtttga cagggatgcg 480  
 ggagaaaaac aagtacttct aaaaccatca aaattcaaca cgcccgaatc tagggcatgg 540  
 cacacgacta atgagacgta taccgtgtgg ggatcaccat ggatatatcg aacgggaacc 600  
 tccgtcaatt gtatagtaga ggaaatggat gcccgctctg tgtttccgta ttcataat ttt 660  
 gcaatggcca atggcgacat cggaacata tctccatttt atggtctatc cccaccagag 720  
 gctgccgcag aacctatggg atatccccag gataatttca aacaactaga tagctat ttt 780  
 tcaatggatt tggacaagcg tcgaaaagca agccttccag tcaagcgtaa ctttctcatc 840  
 acatcacact tcacagttgg gtgggactgg gctccaaaaa ctactcgtgt atgttcaatg 900  
 actaagtgga aagaggtgac tgaaatgttg cgtgcaacag ttaatgggag atacagattt 960  
 atggcccgtg aactttcggc aacgtttatc agtaatacga ctgagtttga tccaaatcgc 1020  
 atcatattag gacaatgtat taaacgcgag gcagaagcag caatcgagca gatatttagg 1080  
 acaaaatata atgacagtca cgtcaagggt ggacatgtac aatatttctt ggctctcggg 1140  
 ggattttatt tagcatatca gcctgttcta tccaaatccc tggctcatat gtacctcaga 1200  
 gaattgatga gagacaacag gaccgatgag atgctcgacc tggtaaaca taagcatgca 1260  
 atttataaga aaaatgctac ctcatgttca cgattgcggc gagatattcg aaatgcacca 1320  
 aatagaaaaa taacattaga cgacaccaca gctattaaat cgacatcgtc tgttcaattc 1380  
 gccatgctcc aatttcttta tgatcatata caaaccata ttaatgatat gtttagtagg 1440  
 attgccacag cttggtgcga attgcagaat agagaacttg ttttatggca cgaagggata 1500  
 aagattaatc cttagcgtac agcgagtgc acattaggaa ggagagtggc tgcaaagatg 1560  
 ttgggggatg tcgctgctgt atcgagctgc actgctatag atgcggaatc cgtcactttg 1620  
 caaaattcta tgcgagttat cacatccact aatacatgtt atagccgacc attggttcta 1680  
 ttttcatatg gagaaaacca aggaaacata cagggacaac tcggtgaaaa caacgagttg 1740  
 cttccaacgc tagaggctgt agagccatgc tcggctaatc atcgtagata ttttctgttt 1800  
 ggatccggtt atgctttatt tgaaaactat aattttgtta agatggtaga cgctgccgat 1860  
 atacagattg ctagcacatt tgtcgagctt aatctaacc tgctagaaga tcgggaaatt 1920  
 ttgcctttat ccgtttacac aaaagaagag ttgcgtgatg ttggtgtatt ggattatgca 1980  
 gaagtagctc gccgcaatca actacatgaa cttaaatttt atgacataaa caaagtaata 2040  
 gaagtggata caaattacgc ggggctgcag gaattcggct gtatgtctat tactaaaaaa 2100  
 gatgcaaacc caaataatgg ccaaacccaa ttagaagcag cgcgaaatgga gttaacagat 2160  
 ctaatcaatg ctaaagcgat gacattagct tctactacaag actatgccaa gattgaagct 2220

```

agtttatcat ctgcttatag tgaagctgaa acagttaaca ataaccttaa tgcaacatta 2280
gaacaactaa aaatggctaa aactaattha gaatcagcca tcaaccaagc taatacggat 2340
aaaacgactt ttgataatga acacccaaat ttagttgaag catacaaagc actaaaaacc 2400
actttagaac aacgtgctac taaccttgaa ggtttgcac caactgctta taatcaaatt 2460
cgcaataatt tagtggatct atacaataaa gctagtagtt taataactaa aacactagat 2520
ccactaaatg ggggaacgct tttagattct aatgagatta ctacagctaa taagaatatt 2580
aataatacgt tatcaactat taatgaacaa aagactaatg ctgatgcatt atctaatagt 2640
tttattaaaa aagtgattca aaataatgaa caaagttttg tagggacttt taaaaacgct 2700
aatgttcaac cttcaaacta cagttttggt gcttttagtg ctgatgtaac acccgtaac 2760
tataaatatg caagaaggac cgtttggaat ggtgatgaac cttcaagtag aattcttgca 2820
aacacgaata gtatcacaga tgtttcttggt atttatagtt tagctggaac aaacacgaag 2880
taccaattta gttttagcaa ctatggtcca tcaactgggt atttatattt cccttataag 2940
ttgggttaaag cagctgatgc taataacggt ggattacaat acaaattaaa taatggaaat 3000
gttcaacaag ttgagtttgc cacttcaact agtgcaaata atactacagc taatccaact 3060
ccagcagttg atgagattaa agttgctaaa atcgttttat cagggtttaag atttggccaa 3120
aacacaatcg aattaagtgt tccaacgggt gaaggaaata tgaataaagt tgcgccaatg 3180
attggcaaca tttatcttag ctcaaataaa aataatgctg ataagatccc cggttaccgt 3240
cgacccggtg catttttata a                                     3261

```

<210> 4

<211> 1086

<212> PRT

<213> hybrid

<400> 4

```

Met His Tyr Phe Arg Arg Asn Cys Ile Phe Phe Leu Ile Val Ile Leu
  1                   5                   10                   15

```

```

Tyr Gly Thr Asn Ser Ser Pro Ser Thr Gln Asn Val Thr Ser Arg Glu
      20                   25                   30

```

```

Val Val Ser Ser Val Gln Leu Ser Glu Glu Glu Ser Thr Phe Tyr Leu
      35                   40                   45

```

```

Cys Pro Pro Pro Val Gly Ser Thr Val Ile Arg Leu Glu Pro Pro Arg
      50                   55                   60

```

```

Lys Cys Pro Glu Pro Arg Lys Ala Thr Glu Trp Gly Glu Gly Ile Ala
      65                   70                   75                   80

```

```

Ile Leu Phe Lys Glu Asn Ile Ser Pro Tyr Lys Phe Lys Val Thr Leu
      85                   90                   95

```

```

Tyr Tyr Lys Asn Ile Ile Gln Thr Thr Thr Trp Thr Gly Thr Thr Tyr
      100                   105                   110

```

```

Arg Gln Ile Thr Asn Arg Tyr Thr Asp Arg Thr Pro Val Ser Ile Glu

```

115	120	125
Glu Ile Thr Asp Leu Ile Asp Gly Lys Gly Arg Cys Ser Ser Lys Ala		
130	135	140
Arg Tyr Leu Arg Asn Asn Val Tyr Val Glu Ala Phe Asp Arg Asp Ala		
145	150	155
Gly Glu Lys Gln Val Leu Leu Lys Pro Ser Lys Phe Asn Thr Pro Glu		
	165	170
Ser Arg Ala Trp His Thr Thr Asn Glu Thr Tyr Thr Val Trp Gly Ser		
	180	185
Pro Trp Ile Tyr Arg Thr Gly Thr Ser Val Asn Cys Ile Val Glu Glu		
	195	200
Met Asp Ala Arg Ser Val Phe Pro Tyr Ser Tyr Phe Ala Met Ala Asn		
	210	215
Gly Asp Ile Ala Asn Ile Ser Pro Phe Tyr Gly Leu Ser Pro Pro Glu		
	225	230
Ala Ala Ala Glu Pro Met Gly Tyr Pro Gln Asp Asn Phe Lys Gln Leu		
	245	250
Asp Ser Tyr Phe Ser Met Asp Leu Asp Lys Arg Arg Lys Ala Ser Leu		
	260	265
Pro Val Lys Arg Asn Phe Leu Ile Thr Ser His Phe Thr Val Gly Trp		
	275	280
Asp Trp Ala Pro Lys Thr Thr Arg Val Cys Ser Met Thr Lys Trp Lys		
	290	295
Glu Val Thr Glu Met Leu Arg Ala Thr Val Asn Gly Arg Tyr Arg Phe		
	305	310
Met Ala Arg Glu Leu Ser Ala Thr Phe Ile Ser Asn Thr Thr Glu Phe		
	325	330
Asp Pro Asn Arg Ile Ile Leu Gly Gln Cys Ile Lys Arg Glu Ala Glu		
	340	345
Ala Ala Ile Glu Gln Ile Phe Arg Thr Lys Tyr Asn Asp Ser His Val		
	355	360
Lys Val Gly His Val Gln Tyr Phe Leu Ala Leu Gly Gly Phe Ile Val		

370		375		380
Ala Tyr Gln Pro Val Leu Ser Lys Ser Leu	Ala His Met Tyr Leu Arg			
385	390	395	400	
Glu Leu Met Arg Asp Asn Arg Thr Asp Glu Met Leu Asp Leu Val Asn				
405	410	415		
Asn Lys His Ala Ile Tyr Lys Lys Asn Ala Thr Ser Leu Ser Arg Leu				
420	425	430		
Arg Arg Asp Ile Arg Asn Ala Pro Asn Arg Lys Ile Thr Leu Asp Asp				
435	440	445		
Thr Thr Ala Ile Lys Ser Thr Ser Ser Val Gln Phe Ala Met Leu Gln				
450	455	460		
Phe Leu Tyr Asp His Ile Gln Thr His Ile Asn Asp Met Phe Ser Arg				
465	470	475	480	
Ile Ala Thr Ala Trp Cys Glu Leu Gln Asn Arg Glu Leu Val Leu Trp				
485	490	495		
His Glu Gly Ile Lys Ile Asn Pro Ser Ala Thr Ala Ser Ala Thr Leu				
500	505	510		
Gly Arg Arg Val Ala Ala Lys Met Leu Gly Asp Val Ala Ala Val Ser				
515	520	525		
Ser Cys Thr Ala Ile Asp Ala Glu Ser Val Thr Leu Gln Asn Ser Met				
530	535	540		
Arg Val Ile Thr Ser Thr Asn Thr Cys Tyr Ser Arg Pro Leu Val Leu				
545	550	555	560	
Phe Ser Tyr Gly Glu Asn Gln Gly Asn Ile Gln Gly Gln Leu Gly Glu				
565	570	575		
Asn Asn Glu Leu Leu Pro Thr Leu Glu Ala Val Glu Pro Cys Ser Ala				
580	585	590		
Asn His Arg Arg Tyr Phe Leu Phe Gly Ser Gly Tyr Ala Leu Phe Glu				
595	600	605		
Asn Tyr Asn Phe Val Lys Met Val Asp Ala Ala Asp Ile Gln Ile Ala				
610	615	620		
Ser Thr Phe Val Glu Leu Asn Leu Thr Leu Leu Glu Asp Arg Glu Ile				

625		630		635		640
Leu Pro Leu Ser Val Tyr Thr Lys Glu Glu Leu Arg Asp Val Gly Val						
		645		650		655
Leu Asp Tyr Ala Glu Val Ala Arg Arg Asn Gln Leu His Glu Leu Lys						
		660		665		670
Phe Tyr Asp Ile Asn Lys Val Ile Glu Val Asp Thr Asn Tyr Ala Gly						
		675		680		685
Leu Gln Glu Phe Gly Cys Met Ser Ile Thr Lys Lys Asp Ala Asn Pro						
		690		695		700
Asn Asn Gly Gln Thr Gln Leu Glu Ala Ala Arg Met Glu Leu Thr Asp						
		705		710		715
						720
Leu Ile Asn Ala Lys Ala Met Thr Leu Ala Ser Leu Gln Asp Tyr Ala						
		725		730		735
Lys Ile Glu Ala Ser Leu Ser Ser Ala Tyr Ser Glu Ala Glu Thr Val						
		740		745		750
Asn Asn Asn Leu Asn Ala Thr Leu Glu Gln Leu Lys Met Ala Lys Thr						
		755		760		765
Asn Leu Glu Ser Ala Ile Asn Gln Ala Asn Thr Asp Lys Thr Thr Phe						
		770		775		780
Asp Asn Glu His Pro Asn Leu Val Glu Ala Tyr Lys Ala Leu Lys Thr						
		785		790		795
						800
Thr Leu Glu Gln Arg Ala Thr Asn Leu Glu Gly Leu Ser Ser Thr Ala						
		805		810		815
Tyr Asn Gln Ile Arg Asn Asn Leu Val Asp Leu Tyr Asn Lys Ala Ser						
		820		825		830
Ser Leu Ile Thr Lys Thr Leu Asp Pro Leu Asn Gly Gly Thr Leu Leu						
		835		840		845
Asp Ser Asn Glu Ile Thr Thr Ala Asn Lys Asn Ile Asn Asn Thr Leu						
		850		855		860
Ser Thr Ile Asn Glu Gln Lys Thr Asn Ala Asp Ala Leu Ser Asn Ser						
		865		870		875
						880
Phe Ile Lys Lys Val Ile Gln Asn Asn Glu Gln Ser Phe Val Gly Thr						



885					890					895						
Phe	Thr	Asn	Ala	Asn	Val	Gln	Pro	Ser	Asn	Tyr	Ser	Phe	Val	Ala	Phe	
900					905					910						
Ser	Ala	Asp	Val	Thr	Pro	Val	Asn	Tyr	Lys	Tyr	Ala	Arg	Arg	Thr	Val	
915					920					925						
Trp	Asn	Gly	Asp	Glu	Pro	Ser	Ser	Arg	Ile	Leu	Ala	Asn	Thr	Asn	Ser	
930					935					940						
Ile	Thr	Asp	Val	Ser	Trp	Ile	Tyr	Ser	Leu	Ala	Gly	Thr	Asn	Thr	Lys	
945					950					955					960	
Tyr	Gln	Phe	Ser	Phe	Ser	Asn	Tyr	Gly	Pro	Ser	Thr	Gly	Tyr	Leu	Tyr	
965					970					975						
Phe	Pro	Tyr	Lys	Leu	Val	Lys	Ala	Ala	Asp	Ala	Asn	Asn	Val	Gly	Leu	
980					985					990						
Gln	Tyr	Lys	Leu	Asn	Asn	Gly	Asn	Val	Gln	Gln	Val	Glu	Phe	Ala	Thr	
995					1000					1005						
Ser	Thr	Ser	Ala	Asn	Asn	Thr	Thr	Ala	Asn	Pro	Thr	Pro	Ala	Val	Asp	
1010					1015					1020						
Glu	Ile	Lys	Val	Ala	Lys	Ile	Val	Leu	Ser	Gly	Leu	Arg	Phe	Gly	Gln	
1025					1030					1035					1040	
Asn	Thr	Ile	Glu	Leu	Ser	Val	Pro	Thr	Gly	Glu	Gly	Asn	Met	Asn	Lys	
1045					1050					1055						
Val	Ala	Pro	Met	Ile	Gly	Asn	Ile	Tyr	Leu	Ser	Ser	Asn	Glu	Asn	Asn	
1060					1065					1070						
Ala	Asp	Lys	Ile	Pro	Gly	Tyr	Arg	Arg	Pro	Gly	Thr	Phe	Leu			
1075					1080					1085						

<210> 5

<211> 86

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modification  
of Davidson's promoter

<400> 5  
tttttttttt ttggcatata aataataata aatacaataa ttaattacgc gtaaaaattg 60  
aaaaactatt ctaatttatt gcactc 86

<210> 6  
<211> 91  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: modification  
of Davidson's promoter

<400> 6  
tttttttttt tttttttttt ggcatataaa taataaatac aataattaat tacgcgtaaa 60  
aattgaaaaa ctattctaatt ttattgcact c 91

<210> 7  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: insertion at  
HindIII-PstI site of modified pUC18

<400> 7  
agctgcccc ccggcaagct tgca 24

<210> 8  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: insertion at  
SalI-EcoRI site of modified pUC18

<400> 8  
tcgacatttt tatgtgtac 19

<210> 9  
<211> 21  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: insertion at  
SacI-EcoRI site of modified pUC18

<400> 9

aatcggccgg gggggccagc t

21